1.a. Full Title:

Co-inheritance of the hemostatic gene polymorphisms and the risk of coronary heart disease: results from the ARIC Study

b. Abbreviated Title (Length 26):

Hemostasis gene polymorphisms and CHD

2. Writing Group (list individual with lead responsibility first):

Lead: Aleksic N.; Wu KK.; Nugent D; Sweetman R; Lopez J; Afshar-Kharghan V; Boerwinkle E.; Ahn C.; and CC representative

Address: UT HOUSTON, INTERNAL MEDICINE-HEMATOLOGY, M.S.B. 5.287 6431 FANNIN HOUSTON TX 77030

Phone: (713) 500-6807 Fax: (713) 500-6810

Electronic Mail Address: alexsic@heart.med.uth.tmc.edu chulahn@heart.med.uth.tmc.edu kkwu@heart.med.uth.tmc.edu

3. Timeline:

Measurements of proposed hemostatic gene polymorphisms in CHD cases and CRS were completed and data are available from database.

Preliminary analysis 08/99
Manuscript preparation 09/99
Circulation to co-authors 10/99
Submission to journal 12/99
4. **Rationale:**

A number of genetic risk factors for the development of CHD have been indicated in the past. Some of these represent polymorphism in genes of proteins that are associated with the process of blood clotting.

Despite of increasing supporting data for role of genetic factors in venous thrombotic disease, data relating the role of genetic factors to risk of arterial thrombosis are sparse and their interpretation is controversial.

The aim of this study is to compare the prevalence of the selected genetic hemostatic polymorphisms in the ARIC case-cohort study subjects and to establish whether the co-inheritance of the several mutant alleles is associated with increased risk of CHD. We propose to evaluate whether the co-inheritance of more than two out of eight hemostatic gene polymorphisms is associated with the increased risk for the future occurrence of thrombosis in the arterial circulation. In addition, we propose to compare the relation of co-inheritance with CHD with regard to the ethnic background. The interaction between genetic prothrombotic risk factors and traditional risk factors will also be evaluated.


4. **Main Hypothesis:**

Presence of multiple genetic hemostatic prothrombotic risk factors increases risk for developing CHD.

5. **Data (variables, time window, source, inclusions/exclusions):**

Data will be sent to the CC and also analyzed locally by Dr Chul Ahn, with supervision from the CC.